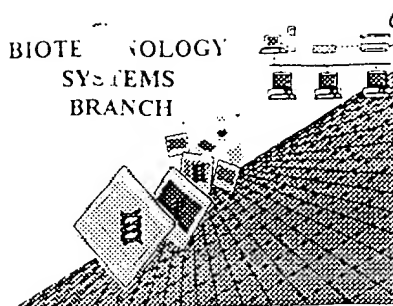


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0280
Oyco.
4-24-01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/816,756

Source: OIPE

Date Processed by STIC: 4-4-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/816,756

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 04/04/2001

PATENT APPLICATION: US/09/816,756

TIME: 14:50:51

Input Set : A:\Coiled-Coil Heterodimer.txt

Output Set: N:\CRF3\04042001\I816756.raw

3 <110> APPLICANT: University of Connecticut
 4 Mayer, Bruce
 6 <120> TITLE OF INVENTION: Coiled-Coil Mediated Heterodimerization Functional
 Interaction Trap

8 <130> FILE REFERENCE: 883933.0062
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/816,756

**Does Not Comply
 Corrected Diskette Needed**

11 <141> CURRENT FILING DATE: 2001-03-24
 13 <150> PRIOR APPLICATION NUMBER: 60/141,896
 14 <151> PRIOR FILING DATE: 1999-06-30
 16 <150> PRIOR APPLICATION NUMBER: PCT/US00/17929
 17 <151> PRIOR FILING DATE: 2000-06-29
 19 <160> NUMBER OF SEQ ID NOS: 2

21 <170> SOFTWARE: PatentIn version 3.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 156

25 <212> TYPE: DNA

26 <213> ORGANISM: Artificial

28 <220> FEATURE:

29 <223> OTHER INFORMATION: Kozak translation start site, followed by an HA-epitope,
 followed

30 by WIN-ZIP-A1 synthetic amphiphatic helix, followed by an infram

31 e Bam HI cloning sit

33 <400> SEQUENCE: 1

34 accatgtacc catacgatgt tccggattac gctggatcta ccatgactgt ggcgcaactg 60

36 gaggaagagg tgaaaaccct tcgtgctcag aattatgaac ttaagtctcg tgtgcagcgc 120

38 ttgcgtgagc aggttgccca gcttgaggga ggtatcc 156

41 <210> SEQ ID NO: 2

42 <211> LENGTH: 165

43 <212> TYPE: DNA

44 <213> ORGANISM: Artificial

46 <220> FEATURE:

47 <223> OTHER INFORMATION: Kozak translation start site, followed by a Myc-epitope,
 followed

48 by a WIN-ZIP-B1 synthetic amphipathic helix, followed by an in-fr

49 ame BamHI cloning sit

51 <400> SEQUENCE: 2

52 accatggagc aaaagctcat ttctgaagag gacttgaatg aaggatctac catgtccggtt 60

54 gacgaactgc aggctgaggt tgaccagctg caggacgaga attacgctct gaagaccaag 120

56 gttgcgcagc tgcgtaaaaa ggtggaaaag ctgggaggag gatcc 165

*Incomplete response for
 <213> as per 1.823(b) of sequence
 rules. See # 11 on Error Summary Sheet*

See above

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/816,756

DATE: 04/04/2001

TIME: 14:50:52

Input Set : A:\Coiled-Coil Heterodimer.txt

Output Set: N:\CRF3\04042001\I816756.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number